

	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

130	*	140	*	150	*	160	*	170	*	180	*	190	*	200	*	210	*	220	*						
AATCATCTGCAGCTGCGAATCATCTGCAGCAGCAAAAGCATCTTCAGGAGCGAGAAAAGCCCCCAATAATGTGAG																									
															ATG	GCA	GTT	GAC	GTC	CGA	ATC	GCT	GCC	TTC	CTG
															Met	Ala	Val	Asp	Val	Arg	Ile	Ala	Ala	Phe	Leu

320	330	340	350	360	370	380	390	400
GTA CTA AAT TTT GAA GGC CAG ACA TGG AGT CAG AGG CCC CTG CTC CCC GAG CCG GAT GAC CTG ATG GAC GCC TAC CAC GTG	Val Leu Asn Phe Glu Gly Gln Thr Trp Ser Gln Arg Pro Leu Leu Pro Ala Pro Glu Arg Asp Leu Cys Met Asp Ala Tyr His Val>							

500	510	520	530	540	550	560	570	580																	
*	*	*	*	*	*	*	*	*																	
TCA	ACT	CCG	TTT	TTA	TCC	GGT	TCG	TAC	AAT	CTG	ATG	CCG	GTC	ATC	AGG	AGA	GTT	GAC	AAC	GGG	AGT	GCA	TCT		
Ser	Thr	Pro	Phe	Ile	Glu	Leu	Pro	Phe	Leu	Pro	Phe	Leu	Ser	Gly	Asn	Val	Arg	Arg	Val	Asp	Asn	Gly	Ser	Ala	Ser>

680	690	700	710	720	730	740	750	760																					
GTG	TCT	CTC	ATC	GTC	AAC	ATA	GAT	GAC	AAC	ATC	ATA	CAA	AAC	TTC	GAG	CCT	TGC	CGG	GTT	CCT	GAA	CTG	GGC	GAG	CCA	GGG			
Val	Ser	Leu	Ala	Ile	Val	Asn	Ile	Asp	Asp	Asn	Ala	Pro	Ile	Ile	Gln	Asn	Phe	Glu	Pro	Cys	Arg	Val	Pro	Glu	Leu	Gly	Glu	Pro	Gly>

860	*	870	*	880	*	890	*	900	*	910	*	920	*	930	*	940	*												
GAG	GAG	ACC	TTC	TAC	ATC	GAA	CGG	ACG	AAT	ATC	CCC	AAC	CAA	TGG	ATG	CTA	AAT	ATG	ACC	ATA	GGC	GTT	AAT	ACC	TCG	CAC	TTC		
Glu	Glu	Thr	Phe	Tyr	Ile	Glu	Arg	Thr	Asn	Ile	Pro	Asn	Gln	Trp	Met	Trp	Leu	Asn	Met	Thr	Ile	Gly	Val	Asn	Thr	Ser	Leu	Asn	Phe>

950	960	970	980	990	1000	1010	1020	1030
*	*	*	*	*	*	*	*	*

Fig 1.

GTC ACC AGT CCG CTG CAT ATA TTC AGC GTG ACA GCC CTG GAC TCG CTC CCG AAC ACC CAC ACG GTG ACT ATG ATG GTG CAA GTG GCG AAT
 Val Thr Ser Pro Leu His Ile Phe Ser Val Thr Ala Leu Asp Ser Leu Pro Asn Thr His Thr Val Thr Met Met Val Gln Val Ala Asn>
 1040 1050 1060 1070 1080 1090 1100 1110 1120
 * * * * *
 GTC AAC AGC CCG CCG CTG TCG CTG GAG ATC TTC GCT GTC CAA CAG TTT GAA GAG AAA TCT TAC CAA AAC TTC ACA GTG AGG GCG ATC
 Val Asn Ser Arg Pro Pro Arg Trp Leu Glu Ile Phe Ala Val Gln Gln Phe Glu Glu Lys Ser Tyr Gln Asn Phe Thr Val Arg Ala Ile>
 1130 1140 1150 1160 1170 1180 1190 1200 1210
 * * * * *
 GAC GGA GAC ACT GAG ATC AAT ATG CCT ATC AAC TAC AGG CTG ATC ACA AAT GAG GAA GAC ACA TTC TTC AGC ATT GAG GCC CTG CCT GGT
 Asp Gly Asp Thr Glu Ile Asn Met Pro Ile Asn Tyr Arg Leu Ile Thr Asn Glu Glu Asp Thr Phe Phe Ser Ile Glu Ala Leu Pro Gly>
 1220 1230 1240 1250 1260 1270 1280 1290 1300
 * * * * *
 GGA AAA AGC GCG GCT GTA TTC CTC GTG TCG CCA ATT GAC CCG GAC ACA CTG CAA CGA GAG GTG TTT CCA CTT ACG ATC GTC GCT TAC AAA
 Gly Lys Ser Gly Ala Val Phe Leu Val Ser Pro Ile Asp Arg Asp Thr Leu Gln Arg Glu Val Phe Pro Leu Thr Ile Val Ala Tyr Lys>
 1310 1320 1330 1340 1350 1360 1370 1380 1390
 * * * * *
 TAT GAT GAG GAG GCC TTC TCC ACA TCA ACA AAC GTG GTC ATC ATT CTG ACA GAC ATC AAC GAC CAA AGA CCT GAA CCT ATA CAC AAG GAA
 Tyr Asp Glu Glu Ala Phe Ser Thr Ser Thr Asn Val Val Ile Ile Val Thr Asp Ile Asn Asp Gln Arg Pro Glu Pro Ile His Lys Glu>
 1400 1410 1420 1430 1440 1450 1460 1470 1480
 * * * * *
 TAT CGA CTG GCA ATC ATG GAG GAG AGC CCG CCC CTG ACC CTC AAC TTC GAT AAA GAA TTC GGA TTT CAT GAT AAG GAT TTA GGT CAA AAC GCT
 Tyr Arg Leu Ala Ile Met Glu Glu Thr Pro Leu Thr Leu Asn Phe Asp Lys Glu Phe Gly Phe His Asp Lys Asp Leu Gly Gln Asn Ala>
 1490 1500 1510 1520 1530 1540 1550 1560 1570
 * * * * *
 CAG TAC ACG GTG CGT CTA GAG AGC GAG GCT CCA GCG GCT GCT GAG GCA TTC TAC ATA GCG CCT GAA GTC GGC TAC CAG CGA CAG ACC
 Gln Tyr Thr Val Arg Leu Glu Ser Val Asp Pro Pro Gly Ala Ala Glu Ala Phe Tyr Ile Ala Pro Glu Val Gly Tyr Gln Arg Gln Thr>
 1580 1590 1600 1610 1620 1630 1640 1650 1660
 * * * * *
 TTC ATC ATG GCC ACC CTC AAT CAC TCC ATG CTG GAT TAC GAA GTG CCA GAG TTT CAG AGT ATT ACG ATT CCG GTG GTA GCG ACC GAC AAC
 Phe Ile Met Gly Thr Leu Asn His Ser Met Leu Asp Tyr Glu Val Pro Glu Phe Gln Ser Ile Thr Ile Arg Val Val Ala Thr Asp Asn>
 1670 1680 1690 1700 1710 1720 1730 1740 1750
 * * * * *
 AAC GAC ACG AGG CAC GTG GCG GTC GCG TTG GTT CAC ATT GAC CTC ATC AAT TGG AAC GAT GAG CAG CCG ATC TTC GAA CAC GCC GTG CAG
 Asn Asp Thr Arg His Val Gly Val Ala Leu Val His Ile Asp Leu Ile Asn Trp Asn Asp Glu Gln Pro Ile Phe Glu His Ala Val Gln>
 1760 1770 1780 1790 1800 1810 1820 1830 1840
 * * * * *
 ACC GTC ACC TTC GAC GAG ACT GAA GCG GAG GCG TTC TTC GTC GCC AAG CCG GTT GCA CAC GAC AGA GAC ATC GCG GAT GTC GTC GAG CAT
 Thr Val Thr Phe Asp Glu Thr Glu Gly Glu Gly Phe Phe Val Ala Lys Ala Val Ala His Asp Arg Asp Ile Gly Asp Val Val Glu His>
 1850 1860 1870 1880 1890 1900 1910 1920 1930
 * * * * *
 ACT TTA TTG GGT AAC GCT GTT AAC TTC CTG ACC ATC GAC AAA CTC ACC GCG GAC ATC CGC GTC TCA GCT AAC GAC TCC TTC AAC TAC CAT
 Thr Leu Leu Gly Asn Ala Val Asn Phe Leu Thr Ile Asp Lys Leu Thr Gly Asp Ile Arg Val Ser Ala Asn Asp Ser Phe Asn Tyr His>
 1940 1950 1960 1970 1980 1990 2000 2010 2020

Fig/607X1

* CGA GAA AGT GAA TTA TTT GTG CAG GTG CCA GGT ACA GAG ACC GTG CCG GAA CCC TTC CAC ACG GCG ACG TCA CAG CTG GTC ATA CGA CTA
 Arg Glu Ser Glu Leu Phe Val Gln Val Arg Ala Thr Asp Thr Leu Gly Glu Pro Phe His Thr Ala Thr Ser Gln Leu Val Ile Arg Leu>
 2030 2040 2050 2060 2070 2080 2090 2100 2110
 * AAT GAC ATC AAC AAC ACG CCA CCC ACC TTA CCG CTG CCT CGA GGC AGT CCC CAA GTG GAG GAG AAC GTG CCT GAT GGC CAC GTC ATC ACC
 Asn Asp Ile Asn Asn Thr Pro Pro Thr Leu Arg Leu Pro Arg Gly Ser Pro Gln Val Glu Glu Asn Val Pro Asp GLY His Val Ile Thr>
 2120 2130 2140 2150 2160 2170 2180 2190 2200
 * CAG GAG TTA CCG GCC ACC GAC CCC GAC ACC ACG GCC GAT CTG CGC TTC GAG ATA AAC TGG GAC ACC TCT TTC GCC ACC AAG CAA GGC CGC
 Gln Glu Leu Arg Ala Thr Asp Thr Thr Ala Asp Leu Arg Phe Glu Ile Asn Trp Asp Thr Ser Phe Ala Thr Lys Gln Gly Arg>
 2210 2220 2230 2240 2250 2260 2270 2280 2290
 * CAG GCT AAC CCC GAC GAG TTT AGG AAT TGC GTG GAA ATC GAG ACC ATC TTC CCC GAG ATT AAC AAC CCG GGA CTG GCT ATC GGC CGC GTT
 Gln Ala Asn Pro Asp Glu Phe Arg Asn Cys Val Glu Ile Glu Thr Ile Phe Pro Glu Ile Asn Asn Arg Gly Leu Ala Ile Gly Arg Val>
 2300 2310 2320 2330 2340 2350 2360 2370 2380
 * GTA CCG CGC GAA ATC AGA CAC AAC GTG ACC ATA GAC TAC GAG GAG TTT GAG GTG CTC TCC CTC ACA GTG AGG GTG CGT GAC CTT AAC ACC
 Val Ala Arg Glu Ile Arg His Asn Val Thr Ile Asp Tyr Glu Glu Phe Glu Val Leu Ser Leu Thr Val Arg Val Arg Asp Leu Asn Thr>
 2390 2400 2410 2420 2430 2440 2450 2460 2470
 * GTC TAC GGA GAC GAC TAC GAC GAA TCG ATG CTC ACA ATA ACT ATA ATC GAT ATG AAC GAC AAC CCG CCG GTG TGG GTG GAG GGC ACT CTG
 Val Tyr Gly Asp Asp Tyr Asp Glu Ser Met Leu Thr Ile Thr Ile Ile Asp Met Asn Asp Asn Ala Pro Val Trp Val Glu Gly Thr Leu>
 2480 2490 2500 2510 2520 2530 2540 2550 2560
 * GAG CAG AAC TTC CGA GTC CGC GAG ATG TCG GCG GGC GCG CTC GTG GTG GGC TCC GTG CGC GAC ATC GAC GGA CCG CTC TAC AAC
 Glu Gln Asn Phe Arg Val Arg Glu Met Ser Ala Gly Glu Val Val Gly Ser Val Arg Ala Asp Asp Ile Asp Gly Pro Leu Tyr Asn>
 2570 2580 2590 2600 2610 2620 2630 2640 2650
 * CAA GTG CGA TAC ACC ATT TTC CCT CCT CGT GGT GAA GAC ACA GAT AAG GAC CTG ATA ATG ATC GAC TTC CTC ACG GGT CAA ATT TCC GTG AAC ACA
 Gln Val Arg Tyr Thr Ile Phe Phe Pro Arg Phe His Leu Tyr Tyr Thr Val Val Ala Ser Asp Arg Cys Ser Thr Glu Asp Pro Ala>
 2660 2670 2680 2690 2700 2710 2720 2730 2740
 * AGC GGC GCG ATC GAC GCG GAT ACT CCT CCA CGC TTC CAC CTC TAC TAT ACA GTG GTC GCT AGT GAC CGA TGC TCG ACA GAA GAT CCT GCA
 Ser Gly Ala Ile Asp Ala Ser Thr Pro Pro Arg Phe His Leu Tyr Tyr Thr Val Val Ala Ser Asp Arg Cys Ser Thr Glu Asp Pro Ala>
 2750 2760 2770 2780 2790 2800 2810 2820 2830
 * GAT TGC CCC CCT GAC CCG ACT TAT TGG GAA ACC GAA GGA AAT ATC ACA ATC CAC ATC ACC GAC ACG AAC AAC AAG GTC CCG CAG GCG GAA
 Asp Cys Pro Pro Asp Pro Thr Tyr Trp Glu Thr Glu Gly Asn Ile Thr Ile His Ile Thr Asp Thr Asn Asn Lys Val Pro Gln Ala Glu>
 2840 2850 2860 2870 2880 2890 2900 2910 2920
 * ACG ACT AAG TTC GAT ACC GTC GTG TAT ATT TAC GAG AAC GCA ACC CAC TTA GAC GAG GTG GTC ACT CTG ATA GCC AGT GAT CTT GAC AGA
 Thr Thr Lys Phe Asp Thr Val Val Tyr Ile Tyr Glu Asn Ala Thr His Leu Asp Glu Val Val Thr Leu Ile Ala Ser Asp Leu Asp Arg>

2930 * 2940 * 2950 * 2960 * 2970 * 2980 * 2990 * 3000 * 3010 *

GAC GAA ATA TAC CAC ACG GTG AGC TAC ATC AAT TAT GCA GTG AAC CCT CGA CTG ATG AAC TTC TTC TCC GTG AAC CGA GAG ACC GGC
 Asp Glu Ile Tyr His **Thr** Val Ser Tyr Val Ile Asn Tyr Ala Val Asn Pro Arg Leu Met Asn Phe Phe Ser Val Asn Arg Glu Thr Gly>

3020 * 3030 * 3040 * 3050 * 3060 * 3070 * 3080 * 3090 * 3100 *

CTG GTG TAC GTG GAC TAT GAG ACC CAG GGT AGT GGC GAG GTG CTG GAC CGT GAT GGT GAT GAA CCA ACG CAC CGT ATC TTC TTC AAC CTC
 Leu Val Tyr Val Asp Tyr Glu Thr Gln Gly Ser Gly Glu Val Leu Asp Arg Asp Gly Asp Glu Pro Thr His Arg Ile Phe Phe Asn Leu>

3110 * 3120 * 3130 * 3140 * 3150 * 3160 * 3170 * 3180 * 3190 *

ATC GAC AAC TTC ATG GGG GAA GGA GAA GGT AAC AGA AAT CAG AAC GAC ACA GAA GTT CTC GTT ATC TTG TTG GAT GTG AAT GAC AAT GCT
 Ile Asp Asn Phe Met Gly Glu Gly Glu Gly Asn Arg Asn Gln Asn Asp Thr Glu Val Leu Val Ile Leu Leu Asp Val Asn Asp Asn Ala>

3200 * 3210 * 3220 * 3230 * 3240 * 3250 * 3260 * 3270 * 3280 *

CCT GAA TTG CCA CCG CCG AGC GAA CTC TCT TGG ACT ATA TCT GAG AAC CTT AAG CAG GGC GTC CGT CTT GAA CCA CAT ATC TTC GCC CCG
 Pro Glu Leu Pro Pro Pro Ser Glu Leu Ser Trp Thr Ile Ser Glu Asn Leu Lys Gln Gly Val Arg Leu Glu Pro His Ile Phe Ala Pro>

3290 * 3300 * 3310 * 3320 * 3330 * 3340 * 3350 * 3360 * 3370 *

GAC CGC GAC GAG CCC GAC ACA GAC AAC TCC AGG GTC GGC TAC GAG ATC CTC AGC ACG GAG CGG GAC ATC GAA GTG CCG GAG CTG
 Asp Arg Asp Glu Pro Asp Thr Asp Asn Ser Arg Val Gly Tyr Glu Ile Leu Asn Leu Ser Thr Glu Arg Asp Ile Glu Val Pro Glu Leu>

3380 * 3390 * 3400 * 3410 * 3420 * 3430 * 3440 * 3450 * 3460 *

TTT GTG ATG ATA CAG ATC GCG AAC GTC ACG GGA GAG CTG GAG ACC GCC ATG GAC CTC AAG GGA TAT TGG GGG ACG TAC GGT ATA CAT ATA
 Phe Val Met Ile Gln Ile Ala Asn Val Thr Gly Glu Leu Glu Thr Ala Met Asp Leu Lys Gly Tyr Trp Gly Thr Tyr Ala Ile **His** Ile>

3470 * 3480 * 3490 * 3500 * 3510 * 3520 * 3530 * 3540 * 3550 *

CGG GCA TTC GAC CAC GGC ATT CCG CAA ATG TCC ATG AAC GAG ACA TAT GAG CTG ATC ATC CAT CCG TTC AAC TAC TAC CCG CCT GAG TTC
Ala Ala Phe Asp His Gly Ile Ile Pro Gln Met Ser Met Asn Glu Thr Tyr Glu Leu Ile Ile His Pro Phe Asn Tyr Tyr Ala Pro Glu Phe>

3560 * 3570 * 3580 * 3590 * 3600 * 3610 * 3620 * 3630 * 3640 *

GTC TTC CCG ACC AAC GAT GCC ATG ATA CGA CTT GCG ACG GAA CGA GCT GTA ATC AAT GGA GTT CTA CCG ACA CTG AAC GGA GAG TTC TTG
 Val Phe Pro Thr Asn Asp Ala Val Ile Arg Leu Ala Arg Glu Arg Ala Val Ile Asn Gly Val Leu Ala Thr Val Asn Gly Glu Phe Leu>

3650 * 3660 * 3670 * 3680 * 3690 * 3700 * 3710 * 3720 * 3730 *

GAG CGG ATA TCG CCG ACT GAT CCG GAC GGA CTC CAC CCG GGC GTC GTC ACC TTC CAA GTG GTA GGC GAT GAG GAA TCA CAA CCG TAC TTT
 Glu Arg Ile Ser Ala Thr Asp Pro Asp Gly Leu His Ala Gly Val Thr Phe Gln Val Val Gly Asp Glu Ser Gln Arg Tyr Phe>

3740 * 3750 * 3760 * 3770 * 3780 * 3790 * 3800 * 3810 * 3820 *

CAA GTA GTT AAC GAT GGC GAG AAC CTC GGC TCG TTG ACG TTA CTG CAA GCC GTT CCA GAG GAG ATC AGG GAG TTC CCG ATA ACG ATT CCG
 Gln Val Val Asn Asp Gly Glu Asn Leu Glu Ser Leu Arg Leu Leu Gln Ala Val Pro Glu Glu Ile Arg Glu Phe Arg Ile Thr Ile Arg>

3830 * 3840 * 3850 * 3860 * 3870 * 3880 * 3890 * 3900 * 3910 *

Py. (1074)

GCT ACA GAC CAG GGA ACG GAC CCA GGA GCG GTG TCG ACC GAC ATG ACC TTC AGA GTT GTT GTG CCC ACG CAA GGA GAA CCT ACA TTC
 Ala Thr Asp Gln Gly Thr Asp Pro Gly Pro Leu Ser Thr Asp Met Thr Phe Arg Val Val Phe Val Pro Thr Gln Gly Glu Pro Arg Phe>
 3920 * 3930 * 3940 * 3950 * 3960 * 3970 * 3980 * 3990 * 4000 *
 GCG TCC TCA GAA CAT GCT GTC GCT TTT ATA GAA AAG AGT GCC GGC ATG GAA GAG TCT CAC CAA CTT CCT CTA GCA CAA GAC ATC AAG AAC
 Ala Ser Ser Glu His Ala Val Ala Phe Ile Glu Lys Ser Ala Gly Met Glu Ser His Gln Leu Pro Leu Ala Gln Asp Ile Lys Asn>
 4010 * 4020 * 4030 * 4040 * 4050 * 4060 * 4070 * 4080 * 4090 *
 CAT CTC TGT GAA GAC GAC TGT CAC AGC ATT TAC TAT CGT ATT ATC GAT GGC AAC AGC GAA GGT CAT TTC GGC CTG CAT CCT GTT CGC AAC
 His Leu Cys Glu Asp Asp Cys His Ser Ile Tyr Tyr Arg Ile Ile Asp Gly Asn Ser Glu Gly His Phe Gly Leu Asp Pro Val Arg Asn>
 4100 * 4110 * 4120 * 4130 * 4140 * 4150 * 4160 * 4170 * 4180 *
 AGG TTG TTC CTG AAG AAA GAG CTG ATA AGG GAA CAA AGT GCC TCC CAC ACT CTG CAA GTG GCG GCT AGT AAC TCG CCC GAT GGT GGC ATT
 Arg Leu Phe Leu Lys Lys Glu Leu Ile Arg Glu Gln Ser Ala Ser His Thr Leu Gln Val Ala Ala Ser Asn Ser Pro Asp Gly Ile>
 4190 * 4200 * 4210 * 4220 * 4230 * 4240 * 4250 * 4260 * 4270 *
 CCA CTT CCT GCT TCC ATC CTT ACT GTC ACT GTT ACC GTG AGG GAG GCA GAC CCT CGT CCA GTG TTT GTG AGG GAA TTG TAC ACC GCA GGG
 Pro Leu Pro Ala Ser Ile Leu Thr Val Thr Val Thr Val Arg Glu Ala Asp Pro Arg Pro Val Phe Val Arg Glu Leu Tyr Thr Ala Gly>
 4280 * 4290 * 4300 * 4310 * 4320 * 4330 * 4340 * 4350 * 4360 *
 ATA TCC ACA GCG GAC TCC ATC GCG AGA GAG CTG CTC AGA TTA CAT GCG ACC CAG TCT GAA GGC TCG GCC ATT ACT TAT GCT ATA GAC TAC
 Ile Ser Thr Ala Asp Ser Ile Gly Arg Glu Leu Leu Arg Leu His Ala Thr Gln Ser Glu Gly Ser Ala Ile Thr Tyr Ala Ile Asp Tyr>
 4370 * 4380 * 4390 * 4400 * 4410 * 4420 * 4430 * 4440 * 4450 *
 GAT ACA ATG GTA GTG GAC CCC AGC CTG GAG GCA GTG AGA CAG TCG GCT TTC GTA CTG AAC GCT CAA ACC GGA GTG CTG ACG CTT AAT ATC
 Asp Thr Met Val Val Asp Pro Ser Leu Glu Ala Val Arg Gln Ser Ala Phe Val Leu Asn Ala Gln Thr Gly Val Leu Thr Leu Asn Ile>
 4460 * 4470 * 4480 * 4490 * 4500 * 4510 * 4520 * 4530 * 4540 *
 CAG CCC ACG GCC ACG ATG CAT GGA CTG TTC AAA TTC GAA GTG ACA GCT ACT GAC ACG GCC GGC GCT CAG GAC CGC ACC GAC GTC ACC GTG
 Gln Pro Thr Ala Thr Met His Gly Leu Phe Lys Phe Glu Val Thr Ala Thr Asp Thr Ala Gly Ala Gln Asp Arg Thr Asp Val Thr Val>
 4550 * 4560 * 4570 * 4580 * 4590 * 4600 * 4610 * 4620 * 4630 *
 TAC GTG GTA TCC TCG CAG AAC CGC GTC TAC TTT GTG TTC GTC AAC ACG CTG CAA CAG GTC GAA GAC AAC AGA GAC TTT ATC GCG GAC ACC
 Tyr Val Val Ser Ser Gln Asn Arg Val Tyr Phe Val Phe Val Asn Thr Leu Gln Gln Val Glu Asp Asn Arg Asp Phe Ile Ala Asp Thr>
 4640 * 4650 * 4660 * 4670 * 4680 * 4690 * 4700 * 4710 * 4720 *
 TTC AGC GCT GGG TTC AAC ATG ACC TGC AAC ATC GAC CAA GTG GTG CCC GCT AAC GAC CCC GTC ACC GGC GTG GCG CTG GAG CAC AGC ACG
 Phe Ser Ala Gly Phe Asn Met Thr Cys Asn Ile Asp Gln Val Val Pro Ala Asn Asp Pro Val Thr Gly Val Ala Leu Glu His Ser Thr>
 4730 * 4740 * 4750 * 4760 * 4770 * 4780 * 4790 * 4800 * 4810 * 4820 * 4830 *
 CAG ATG GCG GCC ACT TCA TAC GGG ACA ACG TAC CCG TAC TCG CTG ATG AGA TAG A ACAGATCCGTAGTACCTAGTCTCTGAGCTCGATACAAACAAG
 Gln Met Ala Ala Thr Ser Tyr Gly Thr Thr Tyr Pro Tyr Ser Leu Met Arg *** XXX>
 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950

Fig. 1 (cont.)

KEY TO UPDATED SEQUENCE:

updated nucleotide number:

Fig. 1 (cont.)

Met	Ala	Val	Asp	Val	Arg	Ile	Ala	Ala	Phe	Leu	Leu	Val	Phe	Ile	Ala	1	5	10	15
Pro	Ala	Val	Leu	Ala	Gln	Glu	Arg	Cys	Gly	Tyr	Met	Thr	Ala	Ile	Pro	20	25	30	
Arg	Leu	Pro	Arg	Pro	Asp	Asn	Leu	Pro	Val	Leu	Asn	Phe	Glu	Gly	Gln	35	40	45	
Thr	Trp	Ser	Gln	Arg	Pro	Leu	Leu	Pro	Ala	Pro	Glu	Arg	Asp	Asp	Leu	50	55	60	
Cys	Met	Asp	Ala	Tyr	His	Val	Ile	Thr	Ala	Asn	Leu	Gly	Thr	Gln	Val	65	70	75	80
Ile	Tyr	Met	Asp	Glu	Glu	Ile	Glu	Asp	Glu	Ile	Thr	Ile	Ala	Ile	Leu	85	90	95	
Asn	Tyr	Asn	Gly	Pro	Ser	Thr	Pro	Phe	Ile	Glu	Leu	Pro	Phe	Leu	Ser	100	105	110	
Gly	Ser	Tyr	Asn	Leu	Leu	Met	Pro	Val	Ile	Arg	Arg	Val	Asp	Asn	Gly	115	120	125	
Ser	Ala	Ser	His	His	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Pro	Gly	Met	130	135	140	
Gln	Gln	Tyr	Met	Phe	Asn	Val	Arg	Val	Asp	Gly	Gln	Ser	Leu	Val	Ala	145	150	155	160
Gly	Val	Ser	Leu	Ala	Ile	Val	Asn	Ile	Asp	Asp	Asn	Ala	Pro	Ile	Ile	165	170	175	
Gln	Asn	Phe	Glu	Pro	Cys	Arg	Val	Pro	Glu	Leu	Gly	Glu	Pro	Gly	Leu	180	185	190	
Thr	Glu	Cys	Thr	Tyr	Gln	Val	Ser	Asp	Ala	Asp	Gly	Arg	Ile	Ser	Thr	195	200	205	
Glu	Phe	Met	Thr	Phe	Arg	Ile	Asp	Ser	Val	Arg	Gly	Asp	Glu	Glu	Thr	210	215	220	
Phe	Tyr	Ile	Glu	Arg	Thr	Asn	Ile	Pro	Asn	Gln	Trp	Met	Trp	Leu	Asn	225	230	235	240
Met	Thr	Ile	Gly	Val	Asn	Thr	Ser	Leu	Asn	Phe	Val	Thr	Ser	Pro	Leu	245	250	255	
His	Ile	Phe	Ser	Val	Thr	Ala	Leu	Asp	Ser	Leu	Pro	Asn	Thr	His	Thr	260	265	270	
Val	Thr	Met	Met	Val	Gln	Val	Ala	Asn	Val	Asn	Ser	Arg	Pro	Pro	Arg	275	280	285	

Trp Leu Glu Ile Phe Ala Val Gln Gln Phe Glu Glu Lys Ser Tyr Gln
 290 295 300

Asn Phe Thr Val Arg Ala Ile Asp Gly Asp Thr Glu Ile Asn Met Pro
 305 310 315 320

Ile Asn Tyr Arg Leu Ile Thr Asn Glu Glu Asp Thr Phe Phe Ser Ile
 325 330 335

Glu Ala Leu Pro Gly Gly Lys Ser Gly Ala Val Phe Leu Val Ser Pro
 340 345 350

Ile Asp Arg Asp Thr Leu Gln Arg Glu Val Phe Pro Leu Thr Ile Val
 355 360 365

Ala Tyr Lys Tyr Asp Glu Glu Ala Phe Ser Thr Ser Thr Asn Val Val
 370 375 380

Ile Ile Val Thr Asp Ile Asn Asp Gln Arg Pro Glu Pro Ile His Lys
 385 390 395 400

Glu Tyr Arg Leu Ala Ile Met Glu Glu Thr Pro Leu Thr Leu Asn Phe
 405 410 415

Asp Lys Glu Phe Gly Phe His Asp Lys Asp Leu Gly Gln Asn Ala Gln
 420 425 430

Tyr Thr Val Arg Leu Glu Ser Val Asp Pro Pro Gly Ala Ala Glu Ala
 435 440 445

Phe Tyr Ile Ala Pro Glu Val Gly Tyr Gln Arg Gln Thr Phe Ile Met
 450 455 460

Gly Thr Leu Asn His Ser Met Leu Asp Tyr Glu Val Pro Glu Phe Gln
 465 470 475 480

Ser Ile Thr Ile Arg Val Val Ala Thr Asp Asn Asn Asp Thr Arg His
 485 490 495

Val Gly Val Ala Leu Val His Ile Asp Leu Ile Asn Trp Asn Asp Glu
 500 505 510

Gln Pro Ile Phe Glu His Ala Val Gln Thr Val Thr Phe Asp Glu Thr
 515 520 525

Glu Gly Glu Gly Phe Phe Val Ala Lys Ala Val Ala His Asp Arg Asp
 530 535 540

Ile Gly Asp Val Val Glu His Thr Leu Leu Gly Asn Ala Val Asn Phe
 545 550 555 560

Leu Thr Ile Asp Lys Leu Thr Gly Asp Ile Arg Val Ser Ala Asn Asp
 565 570 575

Ser Phe Asn Tyr His Arg Glu Ser Glu Leu Phe Val Gln Val Arg Ala	580	585	590
Thr Asp Thr Leu Gly Glu Pro Phe His Thr Ala Thr Ser Gln Leu Val	595	600	605
Ile Arg Leu Asn Asp Ile Asn Asn Thr Pro Pro Thr Leu Arg Leu Pro	610	615	620
Arg Gly Ser Pro Gln Val Glu Glu Asn Val Pro Asp Gly His Val Ile	625	630	635
Thr Gln Glu Leu Arg Ala Thr Asp Pro Asp Thr Thr Ala Asp Leu Arg	645	650	655
Phe Glu Ile Asn Trp Asp Thr Ser Phe Ala Thr Lys Gln Gly Arg Gln	660	665	670
Ala Asn Pro Asp Glu Phe Arg Asn Cys Val Glu Ile Glu Thr Ile Phe	675	680	685
Pro Glu Ile Asn Asn Arg Gly Leu Ala Ile Gly Arg Val Val Ala Arg	690	695	700
Glu Ile Arg His Asn Val Thr Ile Asp Tyr Glu Glu Phe Glu Val Leu	705	710	715
Ser Leu Thr Val Arg Val Arg Asp Leu Asn Thr Val Tyr Gly Asp Asp	725	730	735
Tyr Asp Glu Ser Met Leu Thr Ile Thr Ile Ile Asp Met Asn Asp Asn	740	745	750
Ala Pro Val Trp Val Glu Gly Thr Leu Glu Gln Asn Phe Arg Val Arg	755	760	765
Glu Met Ser Ala Gly Gly Leu Val Val Gly Ser Val Arg Ala Asp Asp	770	775	780
Ile Asp Gly Pro Leu Tyr Asn Gln Val Arg Tyr Thr Ile Phe Pro Arg	785	790	795
Glu Asp Thr Asp Lys Asp Leu Ile Met Ile Asp Phe Leu Thr Gly Gln	805	810	815
Ile Ser Val Asn Thr Ser Gly Ala Ile Asp Ala Asp Thr Pro Pro Arg	820	825	830
Phe His Leu Tyr Tyr Thr Val Val Ala Ser Asp Arg Cys Ser Thr Glu	835	840	845
Asp Pro Ala Asp Cys Pro Pro Asp Pro Thr Tyr Trp Glu Thr Glu Gly	850	855	860

Asn Ile Thr Ile His Ile Thr Asp Thr Asn Asn Lys Val Pro Gln Ala
 865 Cal 8 870 875 880
 Glu Thr Thr Lys Phe Asp Thr Val Val Tyr Ile Tyr Glu Asn Ala Thr
 885 890 895
 His Leu Asp Glu Val Val Thr Leu Ile Ala Ser Asp Leu Asp Arg Asp
 900 905 910
 Glu Ile Tyr His Thr Val Ser Tyr Val Ile Asn Tyr Ala Val Asn Pro
 915 920 925
 Arg Leu Met Asn Phe Phe Ser Val Asn Arg Glu Thr Gly Leu Val Tyr
 930 935 940
 Val Asp Tyr Glu Thr Gln Gly Ser Gly Glu Val Leu Asp Arg Asp Gly
 945 950 955 960
 Asp Glu Pro Thr His Arg Ile Phe Phe Asn Leu Ile Asp Asn Phe Met
 965 970 975
 Gly Glu Gly Glu Gly Asn Arg Asn Gln Asn Asp Thr Glu Val Leu Val
 980 985 Cal 990
 Ile Leu Leu Asp Val Asn Asp Asn Ala Pro Glu Leu Pro Pro Pro Ser
 995 1000 1005
 Glu Leu Ser Trp Thr Ile Ser Glu Asn Leu Lys Gln Gly Val Arg Leu
 1010 1015 1020
 Glu Pro His Ile Phe Ala Pro Asp Arg Asp Glu Pro Asp Thr Asp Asn
 1025 1030 1035 1040
 Ser Arg Val Gly Tyr Glu Ile Leu Asn Leu Ser Thr Glu Arg Asp Ile
 1045 1050 1055
 Glu Val Pro Glu Leu Phe Val Met Ile Gln Ile Ala Asn Val Thr Gly
 1060 1065 1070
 Glu Leu Glu Thr Ala Met Asp Leu Lys Gly Tyr Trp Gly Thr Tyr Ala
 1075 1080 1085
 Ile His Ile Arg Ala Phe Asp His Gly Ile Pro Gln Met Ser Met Asn
 1090 1095 1100
 Glu Thr Tyr Glu Leu Ile Ile His Pro Phe Asn Tyr Tyr Ala Pro Glu
 1105 Cal 10 1110 1115 1120
 Phe Val Phe Pro Thr Asn Asp Ala Val Ile Arg Leu Ala Arg Glu Arg
 1125 1130 1135
 Ala Val Ile Asn Gly Val Leu Ala Thr Val Asn Gly Glu Phe Leu Glu
 1140 1145 1150

Arg Ile Ser Ala Thr Asp Pro Asp Gly Leu His Ala Gly Val Val Thr
 1155 1160 1165
 Phe Gln Val Val Gly Asp Glu Glu Ser Gln Arg Tyr Phe Gln Val Val
 1170 1175 1180
 Asn Asp Gly Glu Asn Leu Gly Ser Leu Arg Leu Leu Gln Ala Val Pro
 1185 1190 1195 1200
 Glu Glu Ile Arg Glu Phe Arg Ile Thr Ile Arg Ala Thr Asp Gln Gly
 1205 1210 1215
 Thr Asp Pro Gly Pro Leu Ser Thr Asp Met Thr Phe Arg Val Val Phe
 1220 1225 *cad II* 1230
 Val Pro Thr Gln Gly Glu Pro Arg Phe Ala Ser Ser Glu His Ala Val
 1235 1240 1245
 Ala Phe Ile Glu Lys Ser Ala Gly Met Glu Glu Ser His Gln Leu Pro
 1250 1255 1260
Leu Ala Gln Asp Ile Lys Asn His Leu Cys Glu Asp Asp Cys His Ser
 1265 1270 1275 1280
 Ile Tyr Tyr Arg Ile Ile Asp Gly Asn Ser Glu Gly His Phe Gly Leu
 1285 1290 1295
 Asp Pro Val Arg Asn Arg Leu Phe Leu Lys Lys Glu Leu Ile Arg Glu
 1300 1305 1310
 Gln Ser Ala Ser His Thr Leu Gln Val Ala Ala Ser Asn Ser Pro Asp
 1315 1320 1325
 Gly Gly Ile Pro Leu Pro Ala Ser Ile Leu Thr Val Thr Val Thr Val
 1330 1335 1340
 Arg Glu Ala Asp Pro Arg Pro Val Phe Val Arg Glu Leu Tyr Thr Ala
 1345 1350 1355 1360
 Gly Ile Ser Thr Ala Asp Ser Ile Gly Arg Glu Leu Leu Arg Leu His
 1365 1370 1375
 Ala Thr Gln Ser Glu Gly Ser Ala Ile Thr Tyr Ala Ile Asp Tyr Asp
 1380 1385 1390
 Thr Met Val Val Asp Pro Ser Leu Glu Ala Val Arg Gln Ser Ala Phe
 1395 1400 1405
Val Leu Asn Ala Gln Thr Gly Val Leu Thr Leu Asn Ile Gln Pro Thr
 1410 1415 1420
Ala Thr Met His Gly Leu Phe Lys Phe Glu Val Thr Ala Thr Asp Thr
 1425 1430 1435 1440

Ala Gly Ala Gln Asp Arg Thr Asp Val Thr Val Tyr Val Val Ser Ser
1445 1450 1455

Gln Asn Arg Val Tyr Phe Val Phe Val Asn Thr Leu Gln Gln Val Glu
1460 1465 1470

Asp Asn Arg Asp Phe Ile Ala Asp Thr Phe Ser Ala Gly Phe Asn Met
1475 1480 1485

Thr Cys Asn Ile Asp Gln Val Val Pro Ala Asn Asp Pro Val Thr Gly
1490 1495 1500

Val Ala Leu Glu His Ser Thr Gln Met Ala Ala Thr Ser Tyr Gly Thr
1505 1510 1515 1520

Thr Tyr Pro Tyr Ser Leu Met Arg
1525

mP EC1	EWMPPIFVP	ENGK	GPFPRLNQL	KSNK	DRG	TKIF	YYSIT	GP	GADSP	PEGV	FTIE	KES
fat EC18	EDTVSFDID	ENAGR	GYVGGIV	ARDAD	L	GNAQL	SYGV	SDW	ANDV	FS	LN	PQT
PC42 EC2	ASPVITLAI	ENTN	GSLFPIPL	ASD	AD	ANEL	QVAED	QEEK	PQL	I	VM	
HPT-1 EC1	IVTENIKAPKV	EMVEN	STPHPIKITQ	VRW	ND	PGAQ	YSLV	DKEL	PRFP	S	IDQE	
BTRcad-1	ITANLGTQVI	YMDE	EIEDEITAIL	NYNG	GP	STP						
BTRcad-2	QNFEP	CRVP	ELGEP									
BTRcad-3	LEIFAVQ	QFE	EKSYQ									
BTRcad-4	IHKEYRL	AIM	EETPL	TLN	F	KEFG						
BTRcad-5	EHAVQT	TFD	ETRGE									
BTRcad-6	RLPRG	SPQVE	ENVPD									
BTRcad-7	VEGTLE	QNFVR	EMSAG									
BTRcad-8	ETTKED	TVVYI	ENATH									
BTRcad-9	PPPS	ELSWTIS	ENLKQ									
BTRcad-10	VFPTN	DAVIRLAR	ERAVIN									
BTRcad-11	ASSEH	AVAFI	EKSA									

Cadherin Consensus Motif ---E.....G.....A.D.....

mP EC1	GWILLHMP	LDREK	I	K	V	E	L	Y	G	H	A	V	S	E	N	G
fat EC18	GMLTLTAR	LDYEE	V	Q	H	Y	I	L	V	Q	A	D	N	G	Q	P
PC42 EC2	GN	LDRE	W	D	S	Y	D	L	T	I	K	V	Q	D	G	G
HPT-1 EC1	GDIYVTOP	LDRE	E	K	D	A	Y	F	A	V	A	K	D	E	Y	G
BTRcad-1	GSASHH	HAR	Q	H	E	L	P	G	M	Q	Y	M	F	N	R	V
BTRcad-2	GDEETFY	IERTN	P	N	Q	W	M	L	N	M	T	I	G	V	N	T
BTRcad-3	GAFLV	LD	R	D	T	L	Q	R	E	V	F	P	L	T	I	V
BTRcad-4	GYQRQTF	IMGTL	NHSM													
BTRcad-5	GDIRVS	ANDSFN														
BTRcad-6	LFPE	INN	INNR	G	L	A	I	G	R	V	V	A	R	E	I	R
BTRcad-7	GSNFR	-HKR	R	I	D	A	N	T	P	P	R	F	L	Y	T	V
BTRcad-8	GLVYVD	YETQ	SG													
BTRcad-9	GVEILN	L	S	T	E	R	D	I	E	V	P	E	L	F	V	M
BTRcad-10	GENL	G	S	L	L	L	Q	A	V	P	E					
BTRcad-11	GLDPVR	N	R	L	F	L	K	K	E							

Cadherin Consensus Motif G.....DRE.....D.ND..P.F

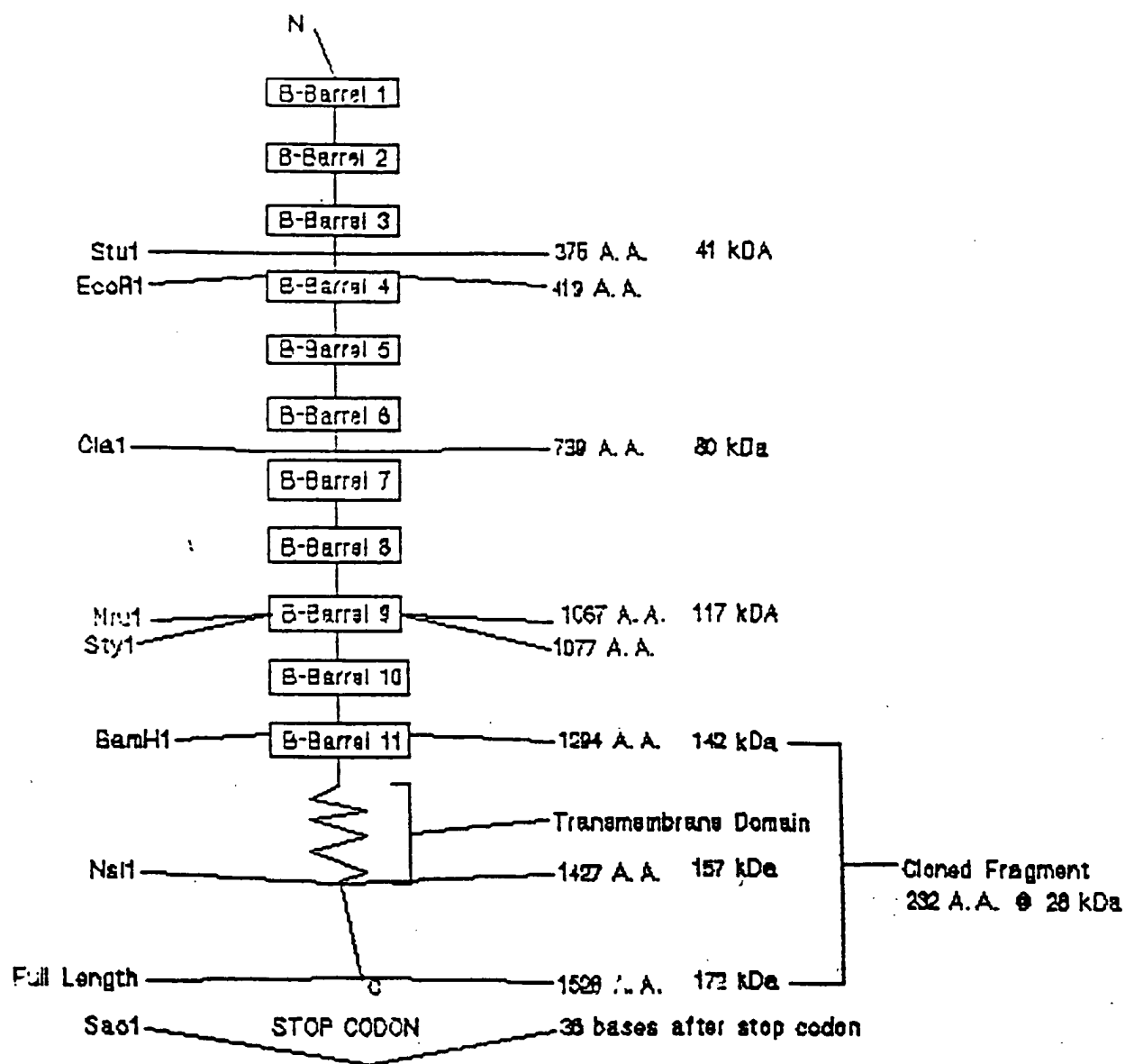


Fig. 3 Block diagram of cadherin-like structure of BT-R₁

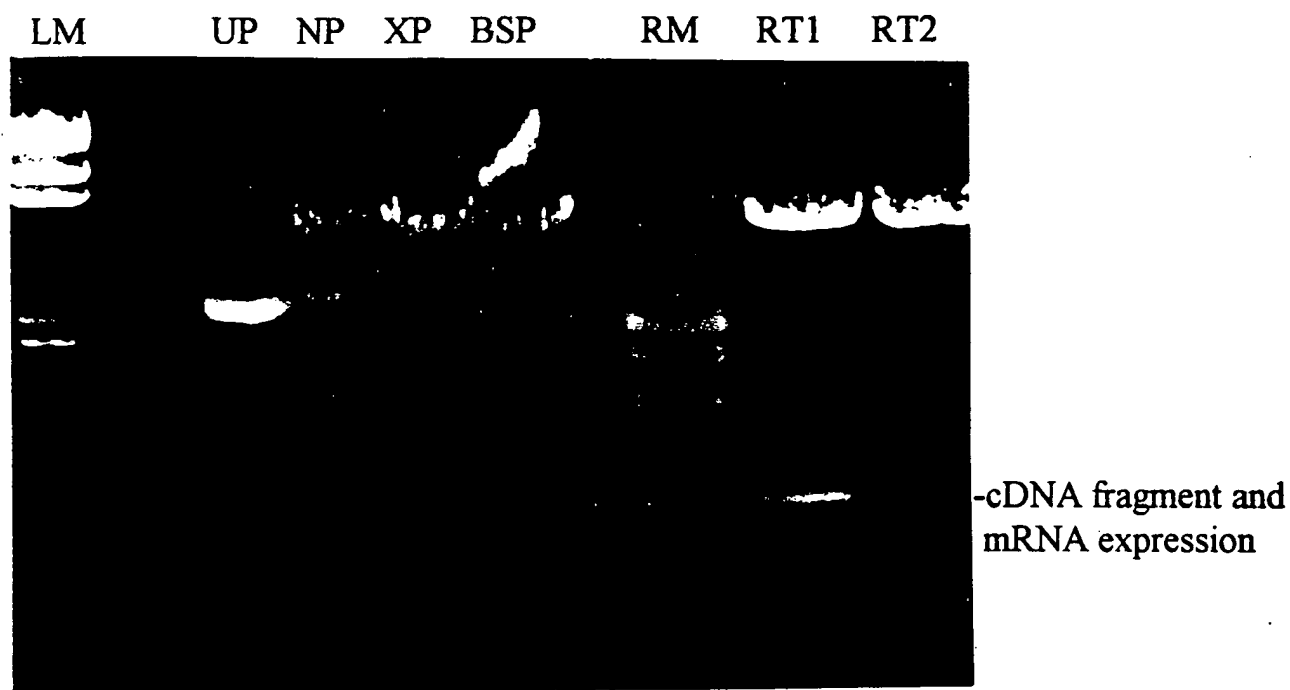


Fig. 4 Clone characterization of BamHI-SacI fragment of BT-R₁. LM is HindIII cut Lambda marker; UP is the uncut plasmid clone; NP is NsiI cut plasmid; XP is XhoI cut plasmid; BSP is BamHI and SacI cut plasmid showing the cloned fragment from BT-R₁; RM is mRNA size marker; and RT1 and RT2 are transcribed mRNAs from the cloned BT-R₁ fragment.

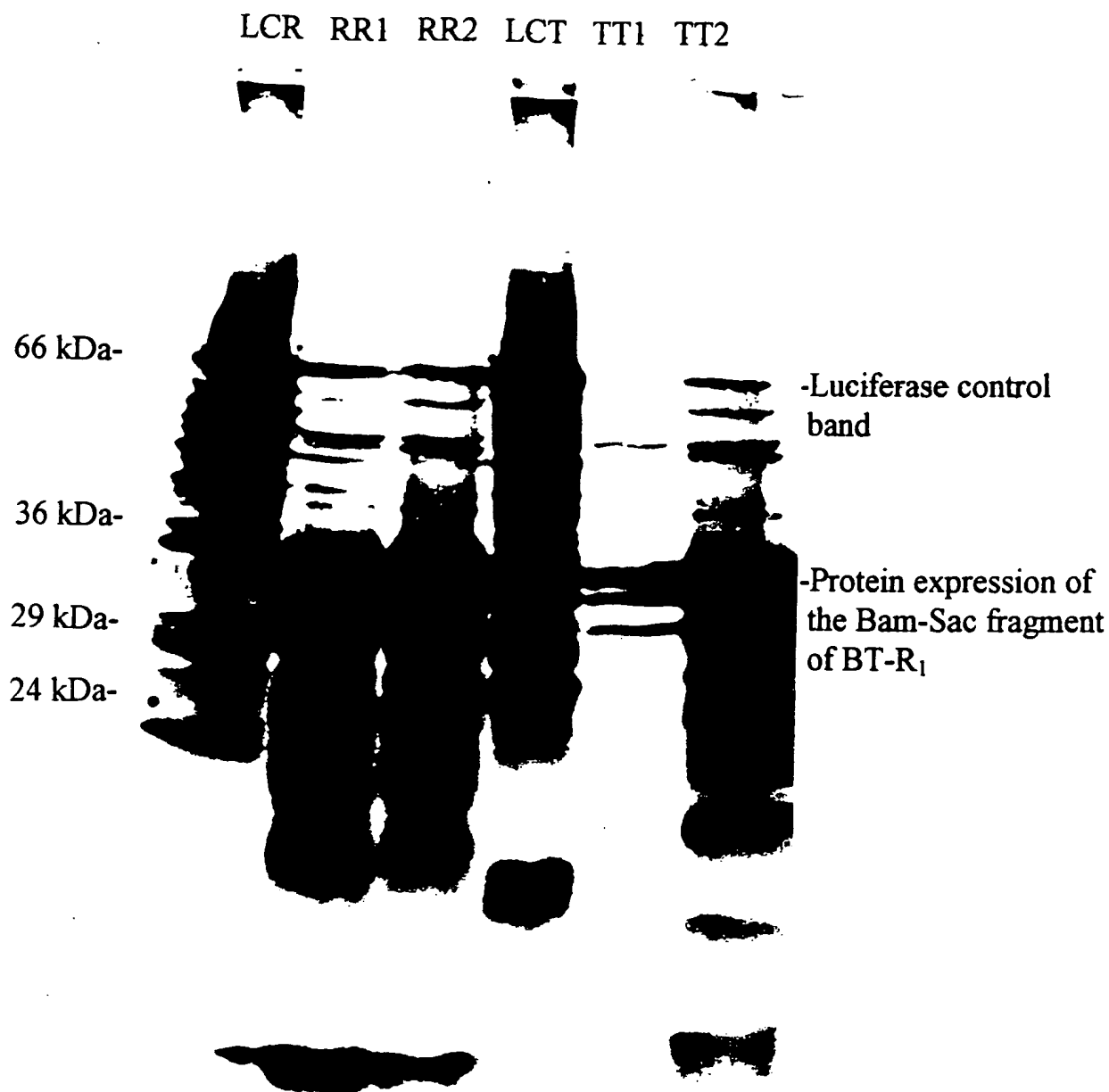


Fig. 5 Detection of protein expression from the plasmid containing the Bam-Sac fragment of BT-R₁ using ³⁵S-methionine as a tag. LCR is a luciferase control mRNA to show that the rabbit reticulocyte lysates are functional; RR1 and RR2 are expression products of the Bam-Sac fragment of BT-R₁ produced in rabbit reticulocytes from mRNA; LCT is a luciferase control plasmid to show that the transcription/translation kit is functional; and TT1 and TT2 are expression products of the Bam-Sac fragment of BT-R₁ produced in a transcription/translation kit.

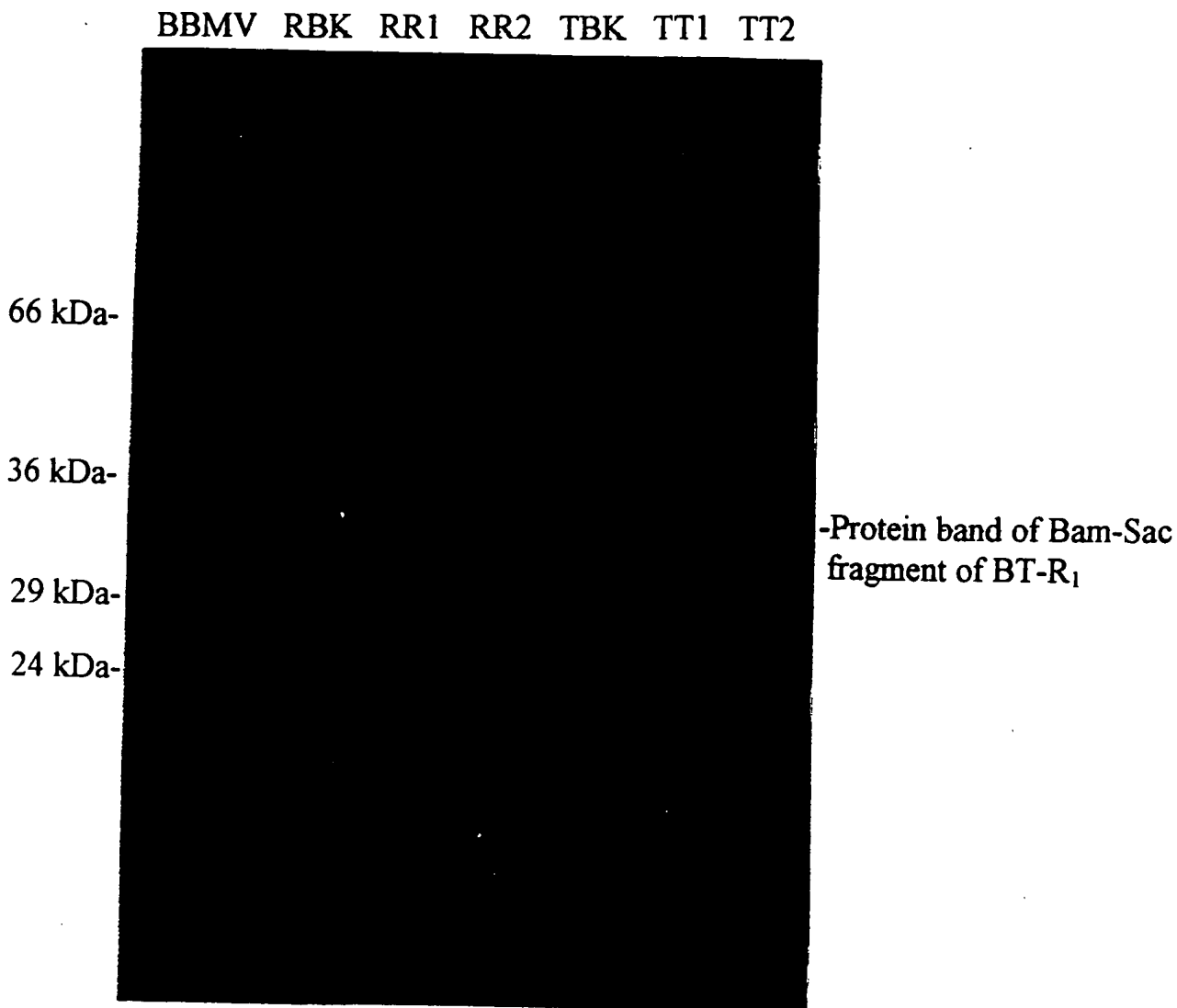


Fig. 6 Radio-blot of the Bam-Sac fragment of BT-R₁ with ¹²⁵I-labeled Cry1Ab. BBMV is the brush border membrane vesicles from the midgut of *M. Sexta* containing the wild-type BT-R₁ receptor protein; RBK is a rabbit reticulocyte blank; RR1 and RR2 are the expression products of the Bam-Sac fragment of BT-R₁ produced in rabbit reticulocytes from mRNA; TBK is a transcription/translation kit blank; TT1 and TT2 are expression products of the Bam-Sac fragment of BT-R₁ produced in a transcription/translation kit. The arrows point to two of the bands.

BBMV proteins

(200µg) from the

Pink bollworm (B)

(*Pectinophora gossypiella*)

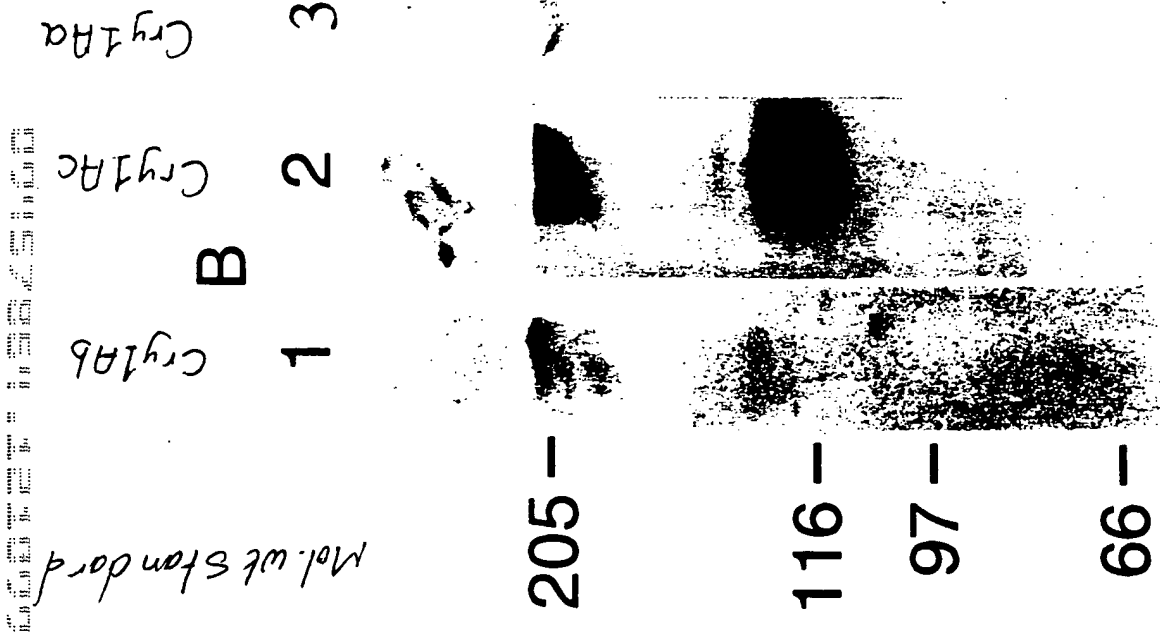
were separated by

7.5% SDS-PAGE, blotted

and probed with 2×10^5 cpm

per ml of 125 I-labeled

Cry toxins.



(can bore)

Fig 7

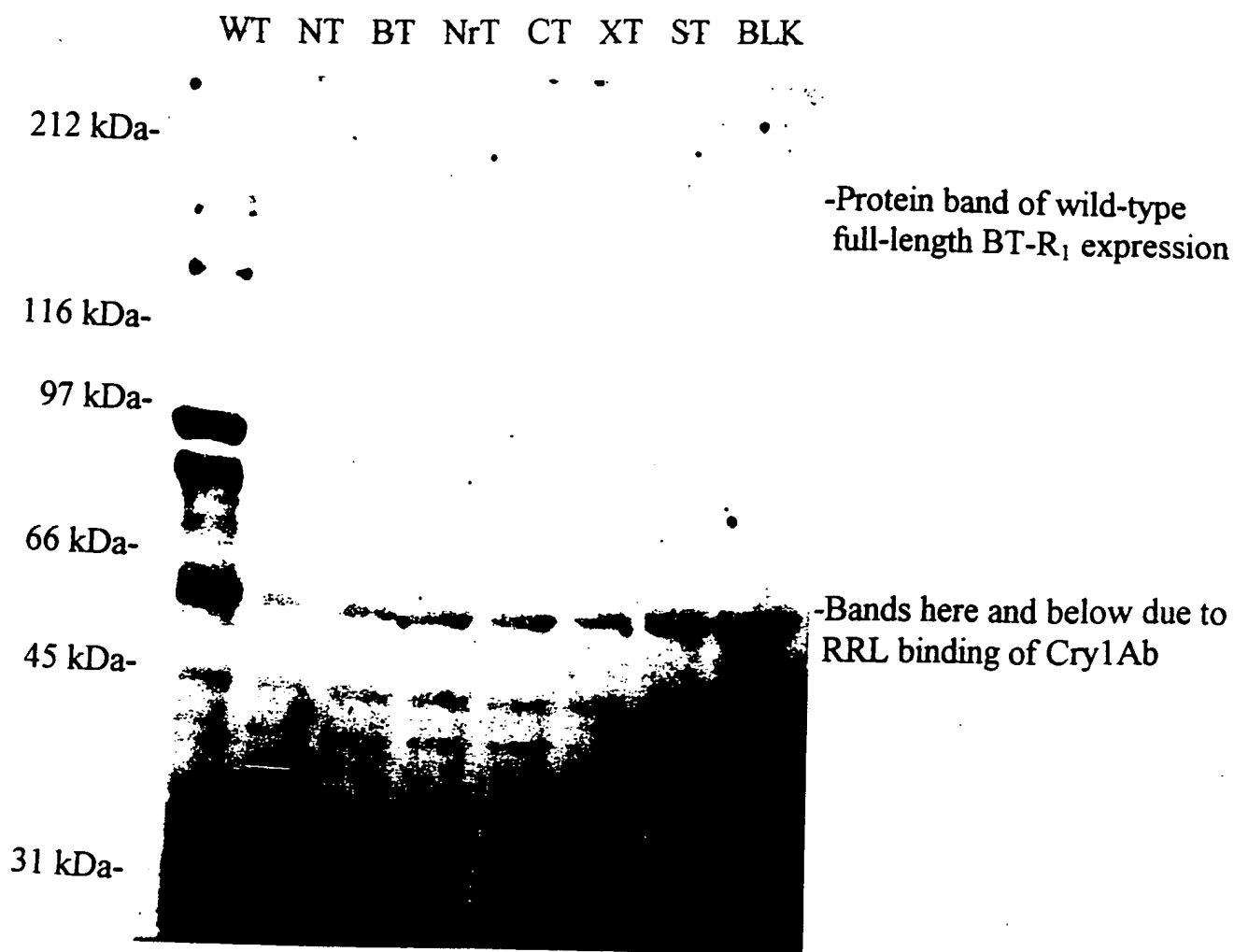


Fig. 8 Radio-blot of BT-R₁ and truncation mutants of BT-R₁ with ¹²⁵I-labeled Cry1Ab. WT is the wild-type full-length BT-R₁ receptor; NT is the truncation mutant resulting from NsiI digestion; BT is the mutant made with BamHI; NrT is the mutant made with NruI; CT is the mutant made with ClaI; XT is the mutant made with XhoI; ST is the mutant made with StuI; and, BLK is rabbit reticulocyte lysates containing only endogenous proteins.